



SEQUENCE LISTING

<110> ITOH, NOBUYA
WAKITA, RYUHEI

<120> PROCESS FOR PRODUCING 3-HYDROXYCYCLOHEXANONE

<130> Q76481

<140> 10/617,034

<141> 2003-07-11

<150> JP 2002-205207

<151> 2002-07-15

<160> 15

<170> PatentIn Ver. 3.2

<210> 1

<211> 348

<212> PRT

<213> Corynebacterium pseudodiphtheriticum

<400> 1

Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr
1 5 10 15

Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
20 25 30

Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro
35 40 45

Glu Glu Gln Tyr Thr Tyr Gly Leu Pro Leu Thr Leu Gly His Glu Gly
50 55 60

Ala Gly Lys Val Ala Ala Val Gly Glu Gly Val Glu Gly Leu Asp Ile
65 70 75 80

Gly Thr Asn Val Val Val Tyr Gly Pro Trp Gly Cys Gly Asn Cys Trp
85 90 95

His Cys Ser Gln Gly Leu Glu Asn Tyr Cys Ser Arg Ala Gln Glu Leu
100 105 110

Gly Ile Asn Pro Pro Gly Leu Gly Ala Pro Gly Ala Leu Ala Glu Phe
115 120 125

Met Ile Val Asp Ser Pro Arg His Leu Val Pro Ile Gly Asp Leu Asp
130 135 140

Pro Val Lys Thr Val Pro Leu Thr Asp Ala Gly Leu Thr Pro Tyr His
145 150 155 160

Ala Ile Lys Arg Ser Leu Pro Lys Leu Arg Gly Gly Ser Tyr Ala Val
165 170 175

Val Ile Gly Thr Gly Gly Leu Gly His Val Ala Ile Gln Leu Leu Arg
180 185 190

His Leu Ser Ala Ala Thr Val Ile Ala Leu Asp Val Ser Ala Asp Lys
195 200 205

Leu Glu Leu Ala Thr Lys Val Gly Ala His Glu Val Val Leu Ser Asp
210 215 220

Lys Asp Ala Ala Glu Asn Val Arg Lys Ile Thr Gly Ser Gln Gly Ala
225 230 235 240

Ala Leu Val Leu Asp Phe Val Gly Tyr Gln Pro Thr Ile Asp Thr Ala
245 250 255

Met Ala Val Ala Gly Val Gly Ser Asp Val Thr Ile Val Gly Ile Gly
260 265 270

Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
275 280 285

Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu
290 295 300

Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Ser Val Glu Thr
305 310 315 320

Phe Ser Leu Asp Asn Gly Ala Glu Ala Tyr Arg Arg Leu Ala Ala Gly
325 330 335

Thr Leu Ser Gly Arg Ala Val Val Val Pro Gly Leu
340 345

<210> 2
<211> 1047
<212> DNA
<213> *Corynebacterium pseudodiphtheriticum*

<220>
<221> CDS
<222> (1)..(1047)

<400> 2
atg aag gcg atc cag tac acg aga atc ggc gcg gaa ccc gaa ctc acg 48
Met Lys Ala Ile Gln Tyr Thr Arg Ile Gly Ala Glu Pro Glu Leu Thr
1 5 10 15

gag att ccc aaa ccc gag ccc ggt cca ggt gaa gtg ctc ctg gaa gtc 96
Glu Ile Pro Lys Pro Glu Pro Gly Pro Gly Glu Val Leu Leu Glu Val
20 25 30

acc gct gct ggc gtc tgc cac tcg gac gac ttc atc atg agc ctg ccc 144
Thr Ala Ala Gly Val Cys His Ser Asp Asp Phe Ile Met Ser Leu Pro
35 40 45

gaa	gag	cag	tac	acc	tac	ggc	ctt	ccg	ctc	acg	ctc	ggc	cac	gaa	ggc	192
Glu	Glu	Gln	Tyr	Thr	Tyr	Gly	Leu	Pro	Leu	Thr	Leu	Gly	His	Glu	Gly	
50						55					60					
gca	ggc	aag	gtc	gcc	gcc	gtc	ggc	gag	ggg	gtc	gaa	ggg	ctc	gac	atc	240
Ala	Gly	Lys	Val	Ala	Ala	Val	Gly	Glu	Gly	Val	Glu	Gly	Leu	Asp	Ile	
65					70					75					80	
gga	acc	aat	gtc	gtc	gtc	tac	ggg	cct	tgg	ggg	tgc	ggc	aac	tgt	tgg	288
Gly	Thr	Asn	Val	Val	Val	Tyr	Gly	Pro	Trp	Gly	Cys	Gly	Asn	Cys	Trp	
			85						90					95		
cac	tgc	tca	caa	gga	ctc	gag	aac	tat	tgc	tct	cgc	gcc	caa	gaa	ctc	336
His	Cys	Ser	Gln	Gly	Leu	Glu	Asn	Tyr	Cys	Ser	Arg	Ala	Gln	Glu	Leu	
			100					105					110			
gga	atc	aat	cct	ccc	ggg	ctc	ggg	gca	ccc	ggc	gcg	ttg	gcc	gag	ttc	384
Gly	Ile	Asn	Pro	Pro	Gly	Leu	Gly	Ala	Pro	Gly	Ala	Leu	Ala	Glu	Phe	
		115					120					125				
atg	atc	gtc	gat	tct	cct	cgc	cac	ctt	gtc	ccg	atc	ggg	gac	ctc	gac	432
Met	Ile	Val	Asp	Ser	Pro	Arg	His	Leu	Val	Pro	Ile	Gly	Asp	Leu	Asp	
	130					135					140					
ccg	gtc	aag	acg	gtg	ccg	ctg	acc	gac	gcc	ggg	ctg	acg	ccg	tat	cac	480
Pro	Val	Lys	Thr	Val	Pro	Leu	Thr	Asp	Ala	Gly	Leu	Thr	Pro	Tyr	His	
145					150					155					160	
gcg	atc	aag	cgt	tct	ctg	ccg	aaa	ctt	cgc	gga	ggc	tcg	tac	gcg	gtt	528
Ala	Ile	Lys	Arg	Ser	Leu	Pro	Lys	Leu	Arg	Gly	Gly	Ser	Tyr	Ala	Val	
			165						170					175		
gtc	att	ggg	acc	ggc	ggg	ctc	ggc	cac	gtc	gct	att	cag	ctc	ctc	cgc	576
Val	Ile	Gly	Thr	Gly	Gly	Leu	Gly	His	Val	Ala	Ile	Gln	Leu	Leu	Arg	
			180					185					190			
cac	ctc	tcg	gcg	gca	acg	gtc	atc	gct	ttg	gac	gtg	agc	gcg	gac	aag	624
His	Leu	Ser	Ala	Ala	Thr	Val	Ile	Ala	Leu	Asp	Val	Ser	Ala	Asp	Lys	
		195					200					205				
ctc	gaa	ctg	gca	acc	aag	gta	ggc	gct	cac	gaa	gtg	gtt	ctg	tcc	gac	672
Leu	Glu	Leu	Ala	Thr	Lys	Val	Gly	Ala	His	Glu	Val	Val	Leu	Ser	Asp	
210						215					220					
aag	gac	gcg	gcc	gag	aac	gtc	cgc	aag	atc	act	gga	agt	caa	ggc	gcc	720
Lys	Asp	Ala	Ala	Glu	Asn	Val	Arg	Lys	Ile	Thr	Gly	Ser	Gln	Gly	Ala	
225					230					235					240	
gca	ttg	gtt	ctc	gac	ttc	gtc	ggc	tac	cag	ccc	acc	atc	gac	acc	gcg	768
Ala	Leu	Val	Leu	Asp	Phe	Val	Gly	Tyr	Gln	Pro	Thr	Ile	Asp	Thr	Ala	
			245					250						255		
atg	gct	gtc	gcc	ggc	gtc	gga	tca	gac	gtc	acg	atc	gtc	ggg	atc	ggg	816
Met	Ala	Val	Ala	Gly	Val	Gly	Ser	Asp	Val	Thr	Ile	Val	Gly	Ile	Gly	
		260						265					270			

gac ggc cag gcc cac gcc aaa gtc ggg ttc ttc caa agt cct tac gag 864
 Asp Gly Gln Ala His Ala Lys Val Gly Phe Phe Gln Ser Pro Tyr Glu
 275 280 285

gct tcg gtg aca gtc ccg tat tgg ggt gcc cgc aac gag ttg atc gaa 912
 Ala Ser Val Thr Val Pro Tyr Trp Gly Ala Arg Asn Glu Leu Ile Glu
 290 295 300

ttg atc gac ctc gcc cac gcc ggc atc ttc gac atc tcg gtg gag acc 960
 Leu Ile Asp Leu Ala His Ala Gly Ile Phe Asp Ile Ser Val Glu Thr
 305 310 315 320

ttc agt ctc gac aac ggt gcc gaa gcg tat cga cga ctg gct gcc gga 1008
 Phe Ser Leu Asp Asn Gly Ala Glu Ala Tyr Arg Arg Leu Ala Ala Gly
 325 330 335

acg ctc agc ggc cgt gcg gtt gtg gtc cct ggt ctg tag 1047
 Thr Leu Ser Gly Arg Ala Val Val Val Pro Gly Leu
 340 345

<210> 3
 <211> 325
 <212> PRT
 <213> Penicillium citrinum

<400> 3
 Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro
 1 5 10 15
 Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
 20 25 30
 Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
 35 40 45
 Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg
 50 55 60
 Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val
 65 70 75 80
 Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp
 85 90 95
 Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met
 100 105 110
 Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu
 115 120 125
 Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr
 130 135 140
 Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp
 145 150 155 160

Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu
 165 170 175
 Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile
 180 185 190
 Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe
 195 200 205
 Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn
 210 215 220
 Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn
 225 230 235 240
 Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala
 245 250 255
 Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro
 260 265 270
 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
 275 280 285
 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
 290 295 300
 Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala
 305 310 315 320
 Lys Asn Leu Ser Ala
 325

<210> 4
 <211> 978
 <212> DNA
 <213> Penicillium citrinum

<220>
 <221> CDS
 <222> (1)..(978)

<400> 4
 atg tct aac gga aag act ttc aca ttg agc aac ggc gtc aag att cct 48
 Met Ser Asn Gly Lys Thr Phe Thr Leu Ser Asn Gly Val Lys Ile Pro
 1 5 10 15
 ggc gtc ggc ttt ggt acc ttc gct agt gaa ggt tcc aag ggc gag acc 96
 Gly Val Gly Phe Gly Thr Phe Ala Ser Glu Gly Ser Lys Gly Glu Thr
 20 25 30
 tat act gct gtc acc act gcc ctg aag acc ggt tac cgt cac ttg gac 144
 Tyr Thr Ala Val Thr Thr Ala Leu Lys Thr Gly Tyr Arg His Leu Asp
 35 40 45

tgt gcc tgg tac tac ctg aac gag ggt gag gtt ggt gag ggt atc cgt	192
Cys Ala Trp Tyr Tyr Leu Asn Glu Gly Glu Val Gly Glu Gly Ile Arg	
50 55 60	
gac ttc ctg aag gag aac ccc tcg gtg aag cgt gag gac atc ttc gtc	240
Asp Phe Leu Lys Glu Asn Pro Ser Val Lys Arg Glu Asp Ile Phe Val	
65 70 75 80	
tgc acc aag gtg tgg aac cac ctc cac cgt tat gag gac gtc ctc tgg	288
Cys Thr Lys Val Trp Asn His Leu His Arg Tyr Glu Asp Val Leu Trp	
85 90 95	
tcc att gac gac tcc ctg aag cgt ctt gga ctt gac tac gtt gat atg	336
Ser Ile Asp Asp Ser Leu Lys Arg Leu Gly Leu Asp Tyr Val Asp Met	
100 105 110	
ttc ctc gtt cac tgg ccc att gct gcc gag aag aat ggc cag ggt gag	384
Phe Leu Val His Trp Pro Ile Ala Ala Glu Lys Asn Gly Gln Gly Glu	
115 120 125	
ccc aag att ggc cct gac ggc aaa tac gtc att ctc aag gac ctg acc	432
Pro Lys Ile Gly Pro Asp Gly Lys Tyr Val Ile Leu Lys Asp Leu Thr	
130 135 140	
gag aac ccc gag ccc aca tgg cgc gct atg gag aag att tat gag gat	480
Glu Asn Pro Glu Pro Thr Trp Arg Ala Met Glu Lys Ile Tyr Glu Asp	
145 150 155 160	
cgc aag gcc agg tcc att ggt gtc tcc aac tgg acc att gcc gac ctt	528
Arg Lys Ala Arg Ser Ile Gly Val Ser Asn Trp Thr Ile Ala Asp Leu	
165 170 175	
gag aag atg tcc aag ttc gcc aag gtc atg cct cac gcc aac cag atc	576
Glu Lys Met Ser Lys Phe Ala Lys Val Met Pro His Ala Asn Gln Ile	
180 185 190	
gag att cac ccc ttc ctg ccc aac gag gag ctg gtg cag tac tgc ttc	624
Glu Ile His Pro Phe Leu Pro Asn Glu Glu Leu Val Gln Tyr Cys Phe	
195 200 205	
tcc aag aac att atg ccc gtg gcc tac tct cct ctg ggc tcg cag aac	672
Ser Lys Asn Ile Met Pro Val Ala Tyr Ser Pro Leu Gly Ser Gln Asn	
210 215 220	
cag gtt ccc acc acc ggt gag cgg gtc agc gag aac aag act ctg aac	720
Gln Val Pro Thr Thr Gly Glu Arg Val Ser Glu Asn Lys Thr Leu Asn	
225 230 235 240	
gag atc gcc gag aag ggc ggc aac acc ctt gct cag gtt ctt att gcc	768
Glu Ile Ala Glu Lys Gly Gly Asn Thr Leu Ala Gln Val Leu Ile Ala	
245 250 255	
tgg ggt ctg cgc cgt ggc tac gtc gtt ctc ccc aag agc tcc aac ccc	816
Trp Gly Leu Arg Arg Gly Tyr Val Val Leu Pro Lys Ser Ser Asn Pro	
260 265 270	

aag cgc att gag tcc aac ttc aag agc att gag ctc tcc gat gcc gac 864
 Lys Arg Ile Glu Ser Asn Phe Lys Ser Ile Glu Leu Ser Asp Ala Asp
 275 280 285

ttt gaa gcc atc aat gcc gtt gcc aag ggt cgt cac ttc cgt ttc gtc 912
 Phe Glu Ala Ile Asn Ala Val Ala Lys Gly Arg His Phe Arg Phe Val
 290 295 300

aac atg aag gat act ttc gga tat gat gtc tgg ccc gag gag acc gcc 960
 Asn Met Lys Asp Thr Phe Gly Tyr Asp Val Trp Pro Glu Glu Thr Ala
 305 310 315 320

aag aac ctg tct gcg tga 978
 Lys Asn Leu Ser Ala
 325

<210> 5
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 5
 gccatggcta tgaaggcgat ccagtac 27

<210> 6
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 6
 cggatccgtc atcgaggcgt gcagctagc 29

<210> 7
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 7
 gccatggcta tgtctaacgg aaagact 27

<210> 8
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 8

cggatccggtt ataatttcgt agagattca

29

<210> 9

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 9

gatcatcata gcaggagtca t

21

<210> 10

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 10

gaattcaaca ccagtcagct c

21

<210> 11

<211> 786

<212> DNA

<213> Bacillus megaterium

<220>

<221> CDS

<222> (1)..(786)

<400> 11

atg	tat	aaa	gat	tta	gaa	gga	aaa	gta	gtt	gtc	ata	aca	ggt	tca	tct	48
Met	Tyr	Lys	Asp	Leu	Glu	Gly	Lys	Val	Val	Val	Ile	Thr	Gly	Ser	Ser	
1				5					10					15		

acc	ggt	tta	gga	aaa	gca	atg	gcg	att	cgt	ttt	gcg	aca	gaa	aaa	gct	96
Thr	Gly	Leu	Gly	Lys	Ala	Met	Ala	Ile	Arg	Phe	Ala	Thr	Glu	Lys	Ala	
		20						25					30			

aaa	gta	gtt	gtg	aac	tat	cgt	tcg	aaa	gaa	gaa	gaa	gct	aac	agc	gtt	144
Lys	Val	Val	Val	Asn	Tyr	Arg	Ser	Lys	Glu	Glu	Glu	Ala	Asn	Ser	Val	
		35					40					45				

tta	gaa	gaa	att	aaa	aaa	gtg	ggc	gga	gag	gct	att	gcc	gtc	aaa	ggt	192
Leu	Glu	Glu	Ile	Lys	Lys	Val	Gly	Gly	Glu	Ala	Ile	Ala	Val	Lys	Gly	
	50					55					60					

gat gta aca gtt gag tct gat gtg atc aat tta gtt caa tct gct att	240
Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile	
65 70 75 80	
aaa gaa ttt gga aag cta gac gtt atg att aat aac gca gga atg gaa	288
Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu	
85 90 95	
aat ccg gtt tcg tct cat gaa atg tct tta agt gat tgg aat aaa gtc	336
Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val	
100 105 110	
att gat acg aac tta acg gga gca ttt tta ggc agc cgt gaa gcg att	384
Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile	
115 120 125	
aaa tat ttt gtg gaa aat gat att aag gga aca gtt att aac atg tcg	432
Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser	
130 135 140	
agt gtt cac gag aaa att cct tgg cca tta ttt gtt cat tac gca gca	480
Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala	
145 150 155 160	
agt aaa ggc gga atg aag ctc atg acc gaa aca ctt gca tta gaa tac	528
Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr	
165 170 175	
gct cca aaa ggt att cgt gta aat aac att gga ccg gga gcg att aat	576
Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn	
180 185 190	
aca ccg att aac gct gag aaa ttt gct gat cct gag cag cgt gca gat	624
Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp	
195 200 205	
gta gaa agc atg att cca atg gga tac att gga gag ccg gaa gaa att	672
Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile	
210 215 220	
gca gcg gtt gct gca tgg cta gct tct tca gag gca agt tat gta aca	720
Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr	
225 230 235 240	
ggg att aca ctc ttt gct gac ggc ggt atg aca cag tac cca tca ttc	768
Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe	
245 250 255	
caa gca gga cgc gga taa	786
Gln Ala Gly Arg Gly	
260	

<210> 12

<211> 261

<212> PRT

<213> Bacillus megaterium

10

<400> 12

```

Met Tyr Lys Asp Leu Glu Gly Lys Val Val Val Ile Thr Gly Ser Ser
 1           5           10           15

Thr Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Ala Thr Glu Lys Ala
      20           25           30

Lys Val Val Val Asn Tyr Arg Ser Lys Glu Glu Glu Ala Asn Ser Val
      35           40           45

Leu Glu Glu Ile Lys Lys Val Gly Gly Glu Ala Ile Ala Val Lys Gly
      50           55           60

Asp Val Thr Val Glu Ser Asp Val Ile Asn Leu Val Gln Ser Ala Ile
      65           70           75           80

Lys Glu Phe Gly Lys Leu Asp Val Met Ile Asn Asn Ala Gly Met Glu
      85           90           95

Asn Pro Val Ser Ser His Glu Met Ser Leu Ser Asp Trp Asn Lys Val
      100          105          110

Ile Asp Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
      115          120          125

Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Thr Val Ile Asn Met Ser
      130          135          140

Ser Val His Glu Lys Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
      145          150          155          160

Ser Lys Gly Gly Met Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
      165          170          175

Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
      180          185          190

Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Glu Gln Arg Ala Asp
      195          200          205

Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
      210          215          220

Ala Ala Val Ala Ala Trp Leu Ala Ser Ser Glu Ala Ser Tyr Val Thr
      225          230          235          240

Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
      245          250          255

Gln Ala Gly Arg Gly
      260

```

<210> 13

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 13

gccatggcta tgtataaaga ttagaa

27

<210> 14

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 14

cggatccggtt atccgctcc tgc

23

<210> 15

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 15

cggatccgag cgccaatac gcaaaccg

28